

Multiple Alignment:

30664188.0.99	1	MHR LI FVYTL I CANFCSC RDT SATPQSA SI KALRNANLRRDESNNHLTDLYR RDET IQVKG	60
VEGF-E	1	--MSLFGLLLT SALAGQRQGTAESNLSSK QFSSNK---EQNGVQDPQ-HERIITVST	54
30664188.0.99	61	NGY VQS PRFPNS YPRN LLLT WR LHS-QENTRIQLVFDNQFGL EEAENDICRYDFVEVEDI	119
VEGF-E	55	NGS IHS PRFPHT YPRN TVLVWR LVAWEENWVLQT FEDERFGLDPEDDICKYDFVEVEEP	114
30664188.0.99	120	SET ST IIRGRWC GHEWPPRIKSR TNQIKITFKSDDYFAKF GKIIYSLL EDFO PAAAS	179
VEGF-E	115	SDG--TILGRWCGSGTWPGKI SKGNQIRIRFVSDEWFPS EFGFCIHNI VMP-----	165
30664188.0.99	180	ETNWESVTSSI SGVSYNSPSV TDP-TLIADA LDKKIAEFDTVED LKVFNPE SWQEDLEN	238
VEGF-E	166	-----QFTEAVS-----PSVLPPSALPLDLLNNAITAFSTLED LIRYLEPERWQLDLED	214
30664188.0.99	239	MYLDTPRYRGRSYHD-RKS-KVDLDRINDDAKRVCSTPRNYSVNI REELKL ANVVFFPRZ	296
VEGF-E	215	LVRPTWQLLGKAFVFGRKSRVWDNLNLT EEVRLVYSTPRNFVSIREELKRTDTIFWPGZ	274
30664188.0.99	297	LLVQR CGGCNCGGCTVN WRSCTNSGKT VKKYHEVLQFE PGHIKRRGRAKTMA LVDIQLDH	356
VEGF-E	275	LLVKRCGGNCACCLHNCNECQGVSPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEH	331
30664188.0.99	357	HERCDCI CSSRPPR	(SEQ ID NO:2) 370
VEGF-E	332	HEECDCV ERGSTGG	(SEQ ID NO:28) 345

FIG. 2.



FIG. 3.

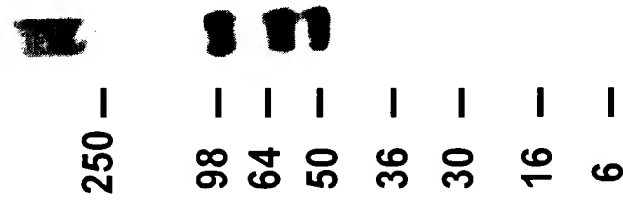


FIG. 4A

IgK 30664188 V5 His



293 Transfection

Ni Affinity Chromatography

Imidazole Elution

FIG. 4B

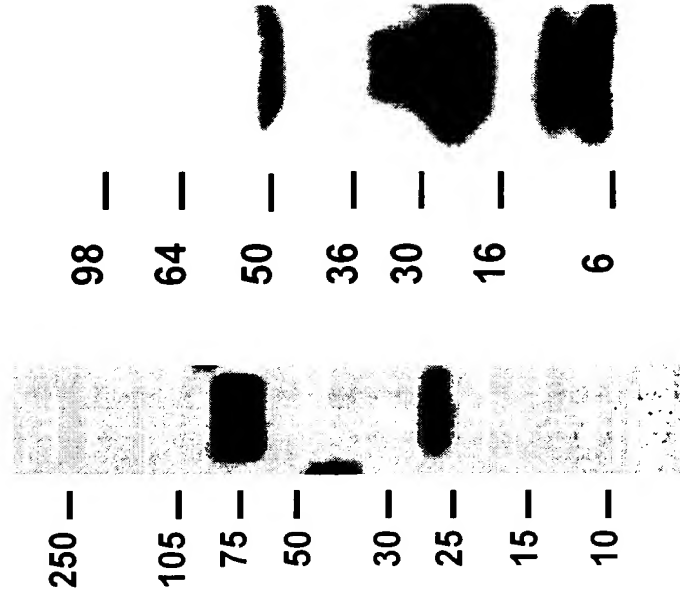


FIG. 5.

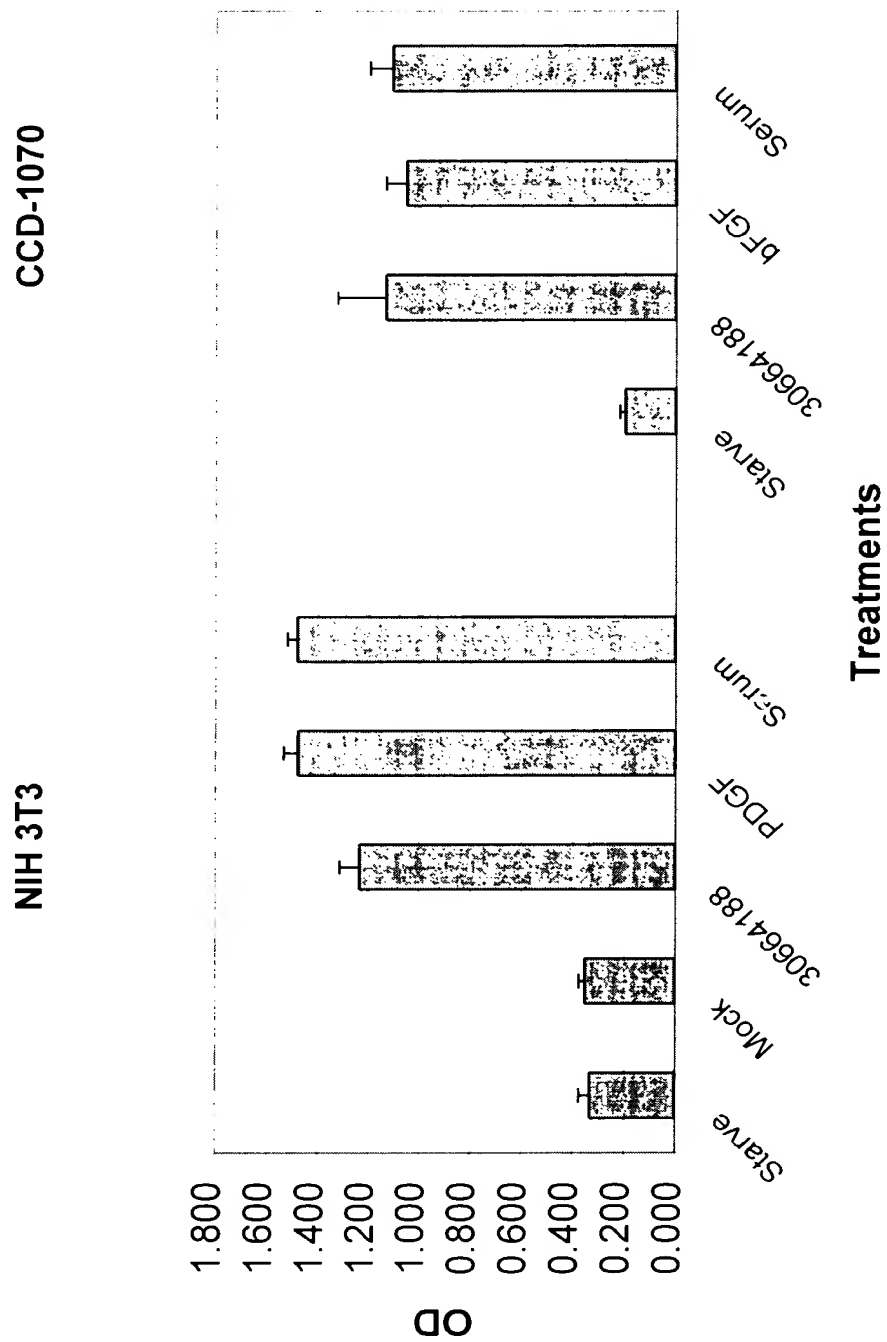


FIG. 6.

BrdU Proliferation NIH 3T3 5-24

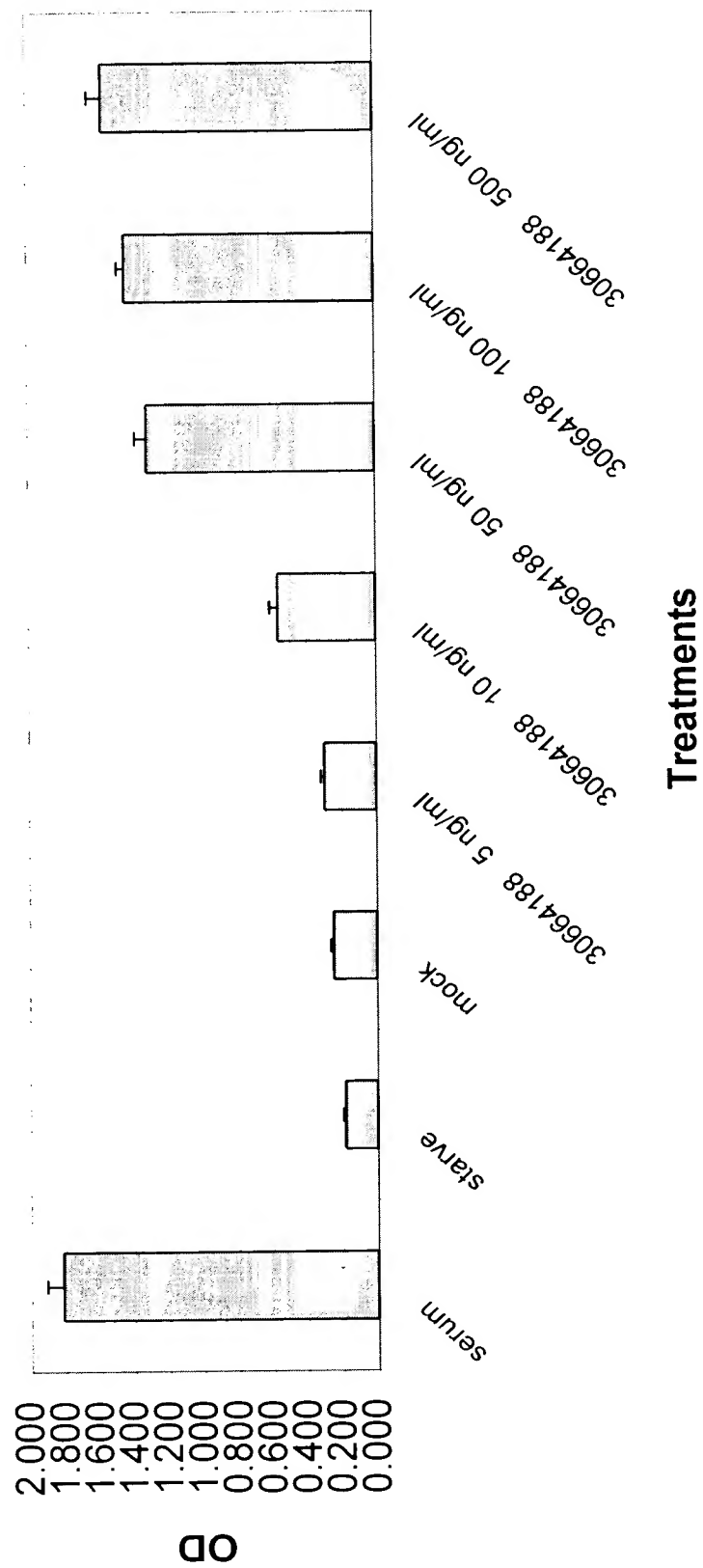


FIG. 7.

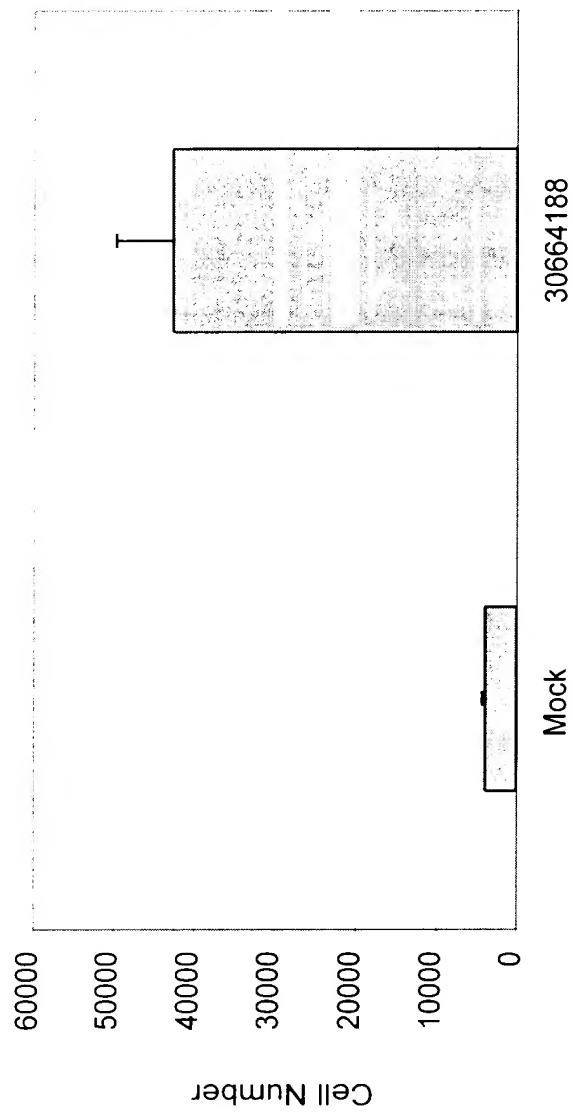


FIG. 9.

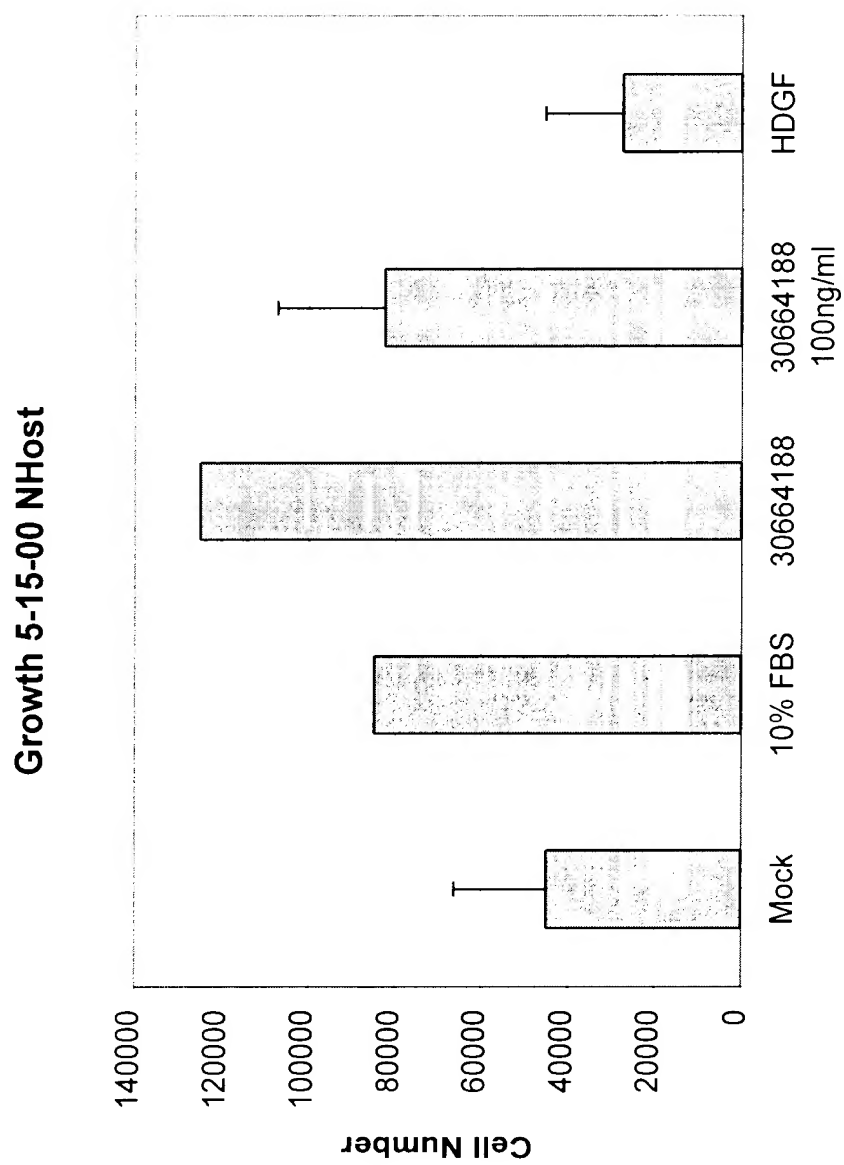


FIG. 10.

FIG. 10A (without serum)

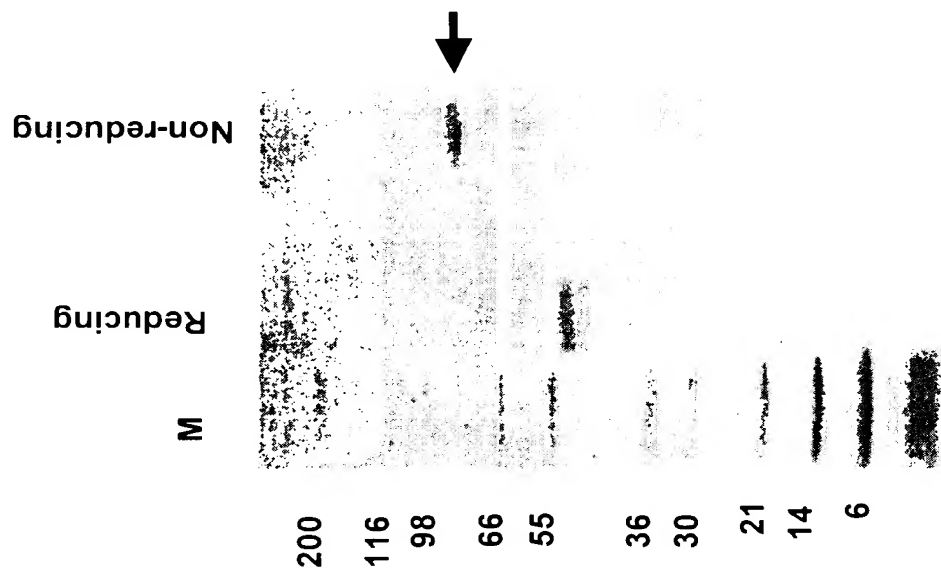


FIG. 10B (with serum)

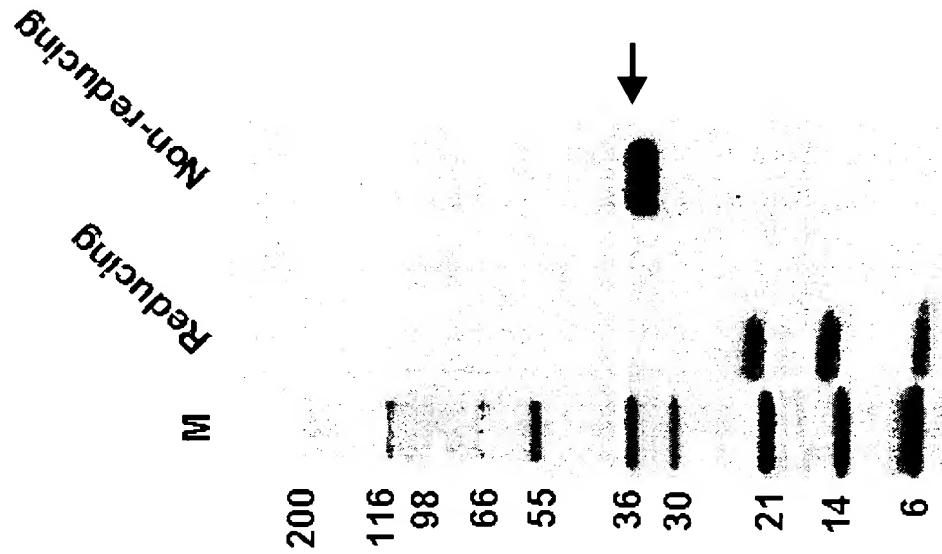


FIG. 11.

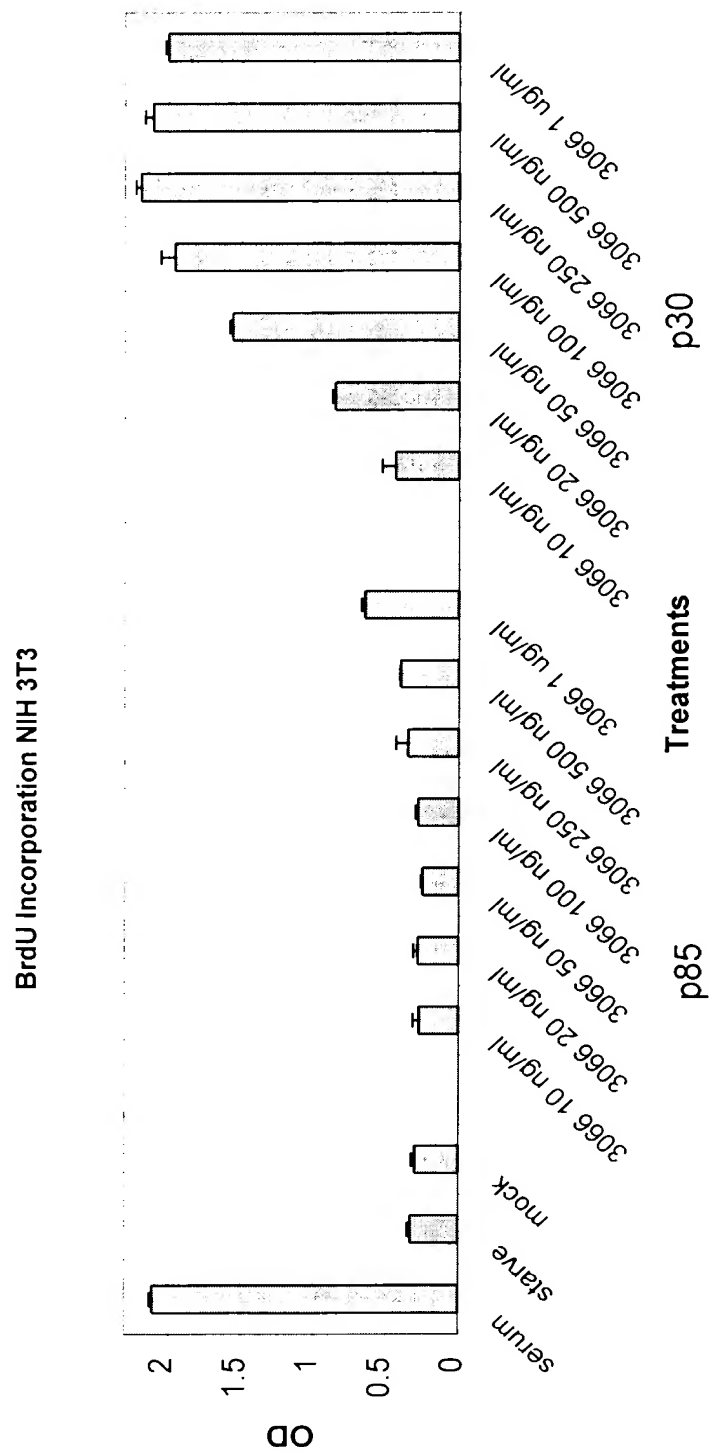


FIG. 12

*

hPDGF D	CTPRNYSVNI-REELKLANVVF--FPRCLLVQRCGGNCGCGTVNWRSTC	
mPDGF D	CTPRNHSVNL-REELKLTNVAF--FPRCLLVQRCGGNCGCGTVNWKSTC	
PDGF C	CTPRNFSVSI-REELKRDTIF--WPGCLLVKRCGGNCACCLHNCNECQC	
PDGF B	CKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCG---CCNNRNVQCRP	
PDGF A	CKTRTVIYEIPRSQVDPTSANFLIWPPCVEVKRCTG---CCNTSSVKCQP	
hPDGF D	NS---GKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDC	(SEQ ID NO:15)
mPDGF D	SS---GKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDC	(SEQ ID NO:16)
PDGF C	VP---SKVTKKYHEVLQLRPKTGVRGLH-KSLTDVA--LEHHEECDC	(SEQ ID NO:17)
PDGF B	TQVQLRPVQVRKIEIVRKKPIF-----KKAT-VT---LEDHLACKC	(SEQ ID NO:18)
PDGF A	SRVHHRSVKVAKVEYVRKKPKL-----KEVQ-VR---LEEHLECAC	(SEQ ID NO:19)

FIG. 13



1  Exon 1
 CGCAGGGGGGGGGGGGGGGTGGGTGGGGGGGAGCAGAAAGGGGGTTTTTTCTTGGAGGGAGCGCTGTCTCTAGTGGCTGATCCCA
 81  AATGACCGGGTTCATCTTTGTCTACACTCTAATCTGGGCAAACTTTTGCAGCTGTGGGGACACTTCTGCAACCGGGCAGA
 M H R L I F V Y T L I C A N F C S C R D T S A T P Q S
 GGGCATCCATCAAAAGCTTTGGGCAACGGCAACCTCAGGGGAGATGAGAGCAATCACTCAGAGACTTGTACCGAAGAGAT
 161 A S I K A L R N A N L R R D E S N H L T D L Y R R D
 GAGACCATCCAGGTGAAAGGAAACGGCTACGTGGCAGAGTCTAGATTCCCGAACAGCTACCGCCAGGAACCTGCTCTGAC
 241 E T I Q V K G N G Y V Q S P R F P N S Y P R N L L L T
 ATGGGGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGAAAATG
 321 W R L H S Q E N T P I Q L V F D N Q F G L E E A E N D
 ATATCTGTATGATGATTTTGTGGAGTTGAAGATATATCCGAAACCACTACCATATTATTAGAGGAGGATGGTGTGGACAC
 401 I C R Y D F V E V E D I S E T S T I I R G R W C G H
 AAGGAAGTTTCTCCAAAGGATAAAATCAAGAAACGAACCAATTAATAATCAACATTCAAGTCCGATGACTACTTTTGTGGCTAA
 481 K E V P P R I K S R T N Q I K I T F K S D D Y F V A K
 ACGTGGATTCAAGATTTATTATCTTTGCTGGAAGATTTCCAAACCGCAGCAGCTTCAGAGACCAACTGGGAATCTGTCA
 561 P G F K I Y Y S L L E D F Q P A A A S E T N W E S T
 CAAGCTCTATTTCAGGGGTATCTTATAACTCTCCATCAGTAACGGATCCCACTCTGATTGGGGATGCTCTGGACAAAAAA
 641 S S I S G V S Y N S P S V T D P T L I A D A L D K K
 ATTGCAGAATTTGATACAGTGGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCAATGGCAAGAAGATCTTGAGAATATGTA
 721 I A E F D T V E D L L K Y F N P E S W Q E D L E N M Y
 TCTGGACACCCCTCTGGTATGGAGGCGAGTCCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATG
 801 L D T P R Y R G R S Y H D R K S K V D L D R L N D D A
 CCAAGCGTTTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGGCAATGTGGTCTTTCTTT
 881 K R Y S C T P R N Y S V N I R E E L K L A N V V F F
 CCAAGTTGGCTCTCTCTGTCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACTGTCAACTGGAGGCTCTGCACATGCAATTC
 961 P R C L L V Q R C G G N C G C G T V N W R S C T C N S
 AGGGAAAAACCGTGAAAAAGTATCATGAGTATTACAGTTTGGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCA
 1041 G K T V K K Y H E V L Q F E P G H I K R R G R A K T M
 TGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATGTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAAT
 1121 A L V D I Q L D H H E R C D C I C S S R P P R (SEQ ID NO:20)
 GTGCACATCCTTACATTAAGCGTGAAAGAACCTTTAGTTTAAAGGAGGGTGAGATAAGAGACCGCTTTTCTACCCAGCAACC
 1201 AAACCTTACTACTAGCCTGCAATGCAATGAACACAAGTGGTGTGCTGAGTCTCAGCCTTGTCTTTGTTAATGCCATGGCAAGT
 1281 AGAAAGGTATATCATCAACTCTATACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTATATATGCACAA
 1361 ACACACACAGAAATATATTTCATGTCTATGTGTATATAGATCAAAATGTTTTTTTTTGGTATATATAACCGAGGTACACCAGAG
 1441 CTTACATATGTTTGAGTTAGACTCTTAAATCTTTGGCAAAATAAGGGATGGTCAAAATATATGAAACATGTCTTTAGAA
 1521 AATTTAGGAGATAAATTTATTTTTAAATTTTGAACACAAAACAATTTGAATCTTGTCTCTTTAAAGAAAGCATCTTGT
 1601 ATATTAATAATCAAAAGATGAGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:21)
 1681

FIG. 14

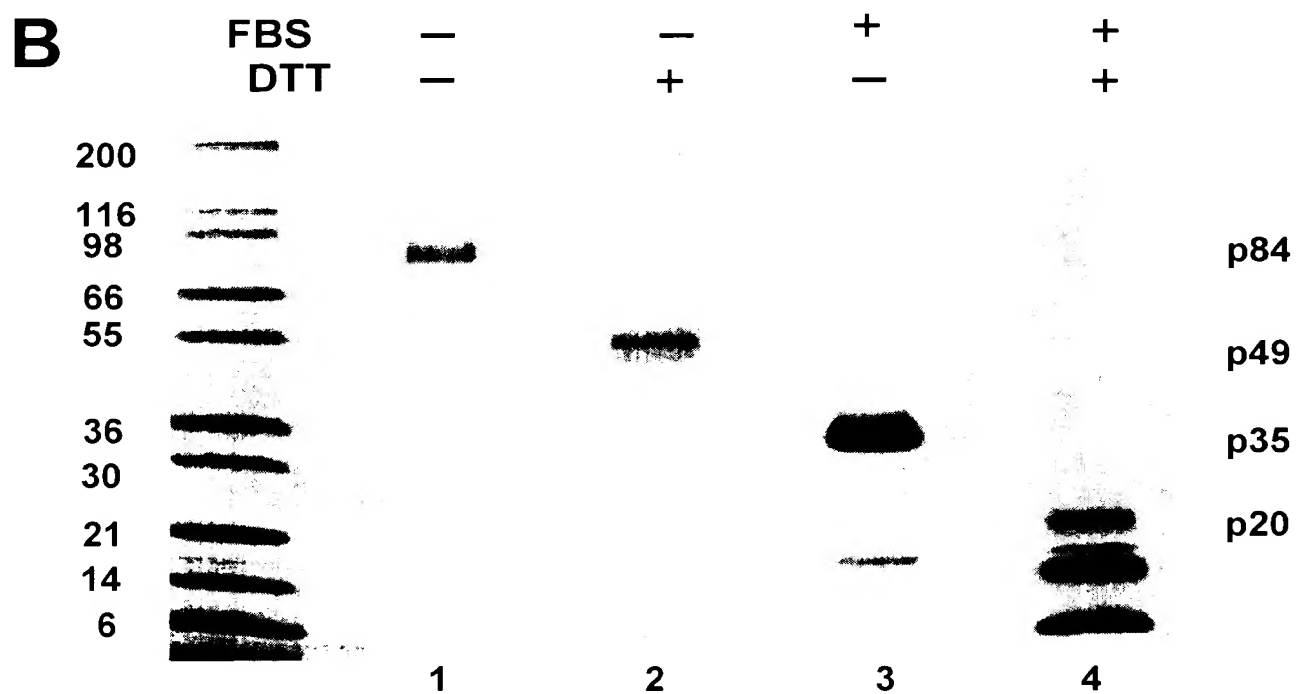
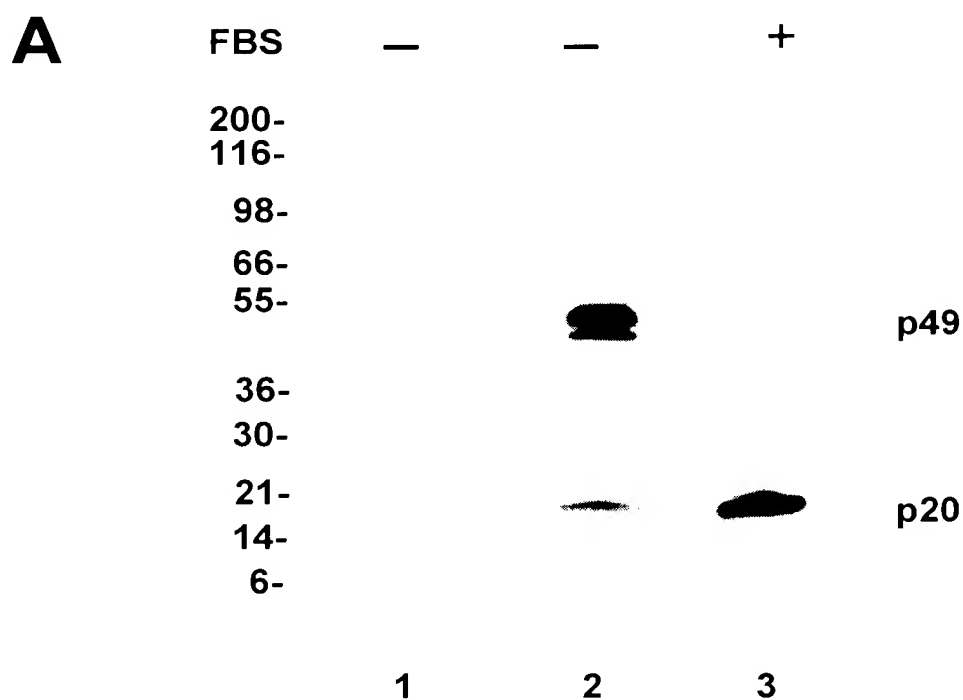


FIG. 15

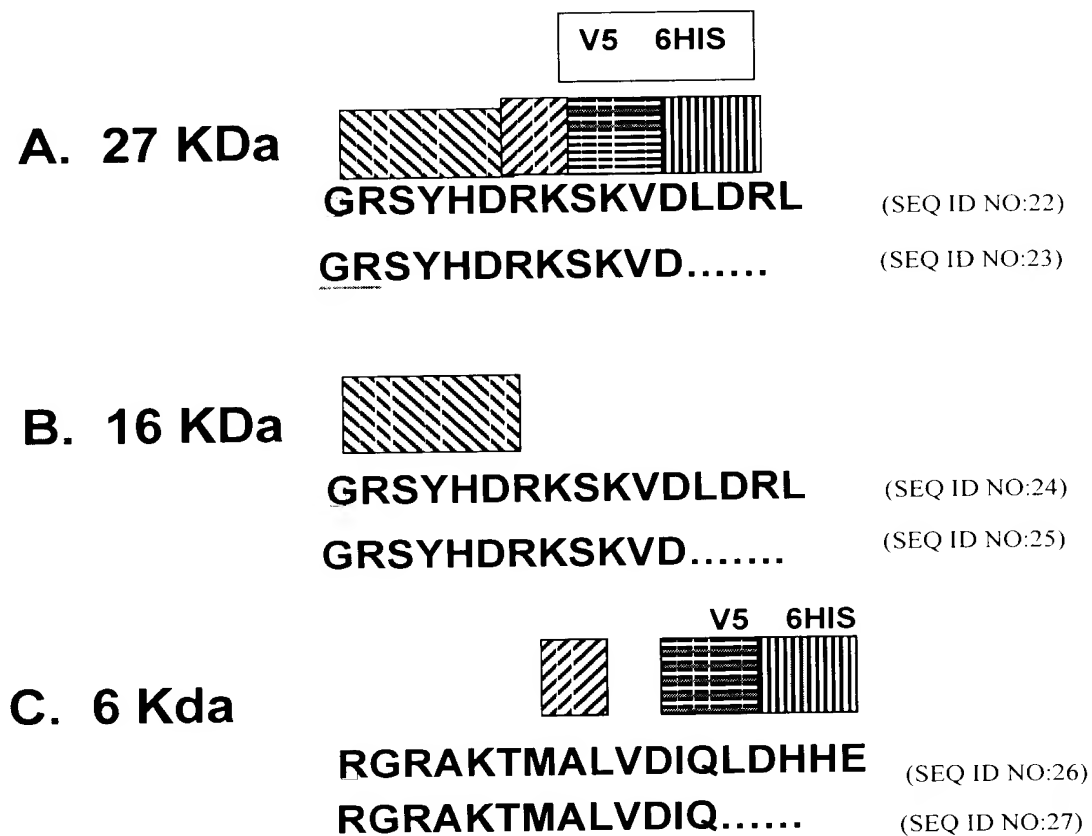


FIG. 16

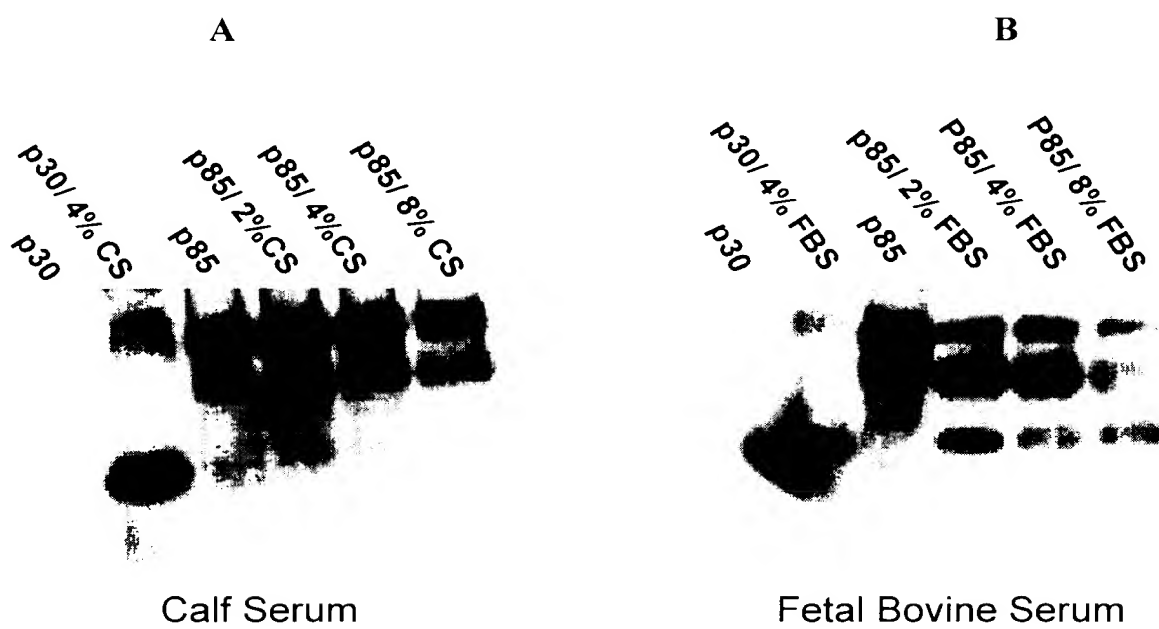


FIG. 17

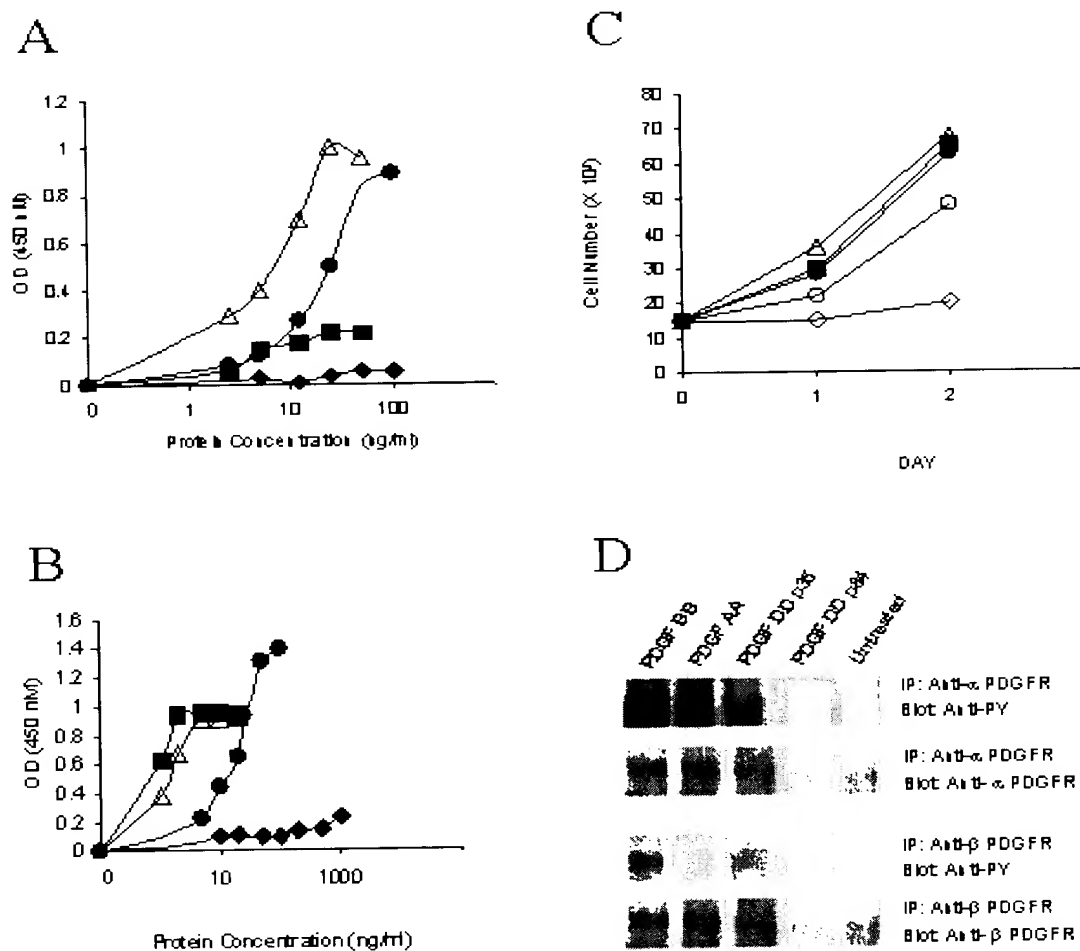
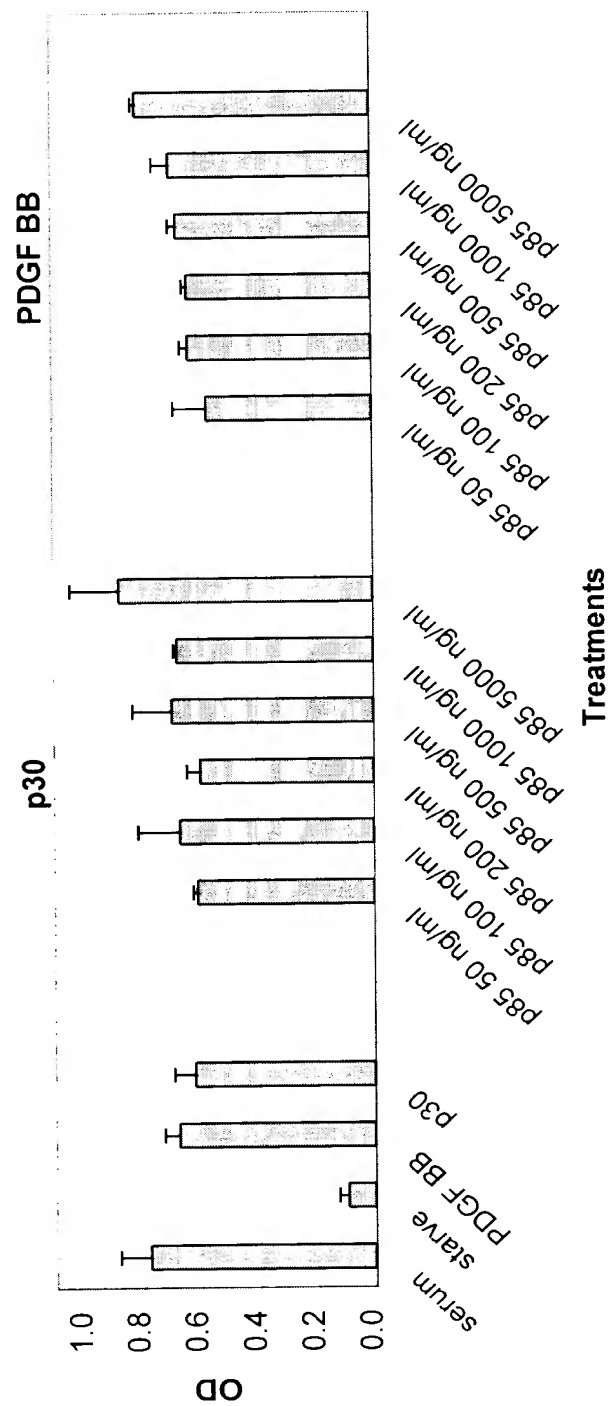


FIG. 18

Competition of 30664188 p30 or PDGF BB by 30664188 p85



A

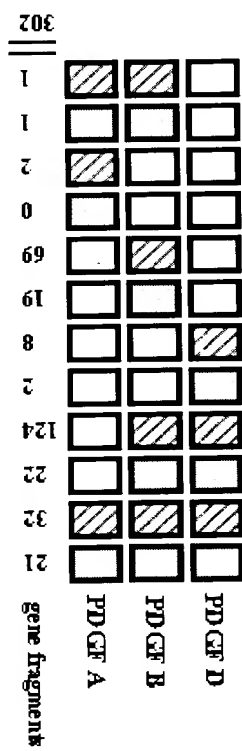


FIG. 19

FIG. 20

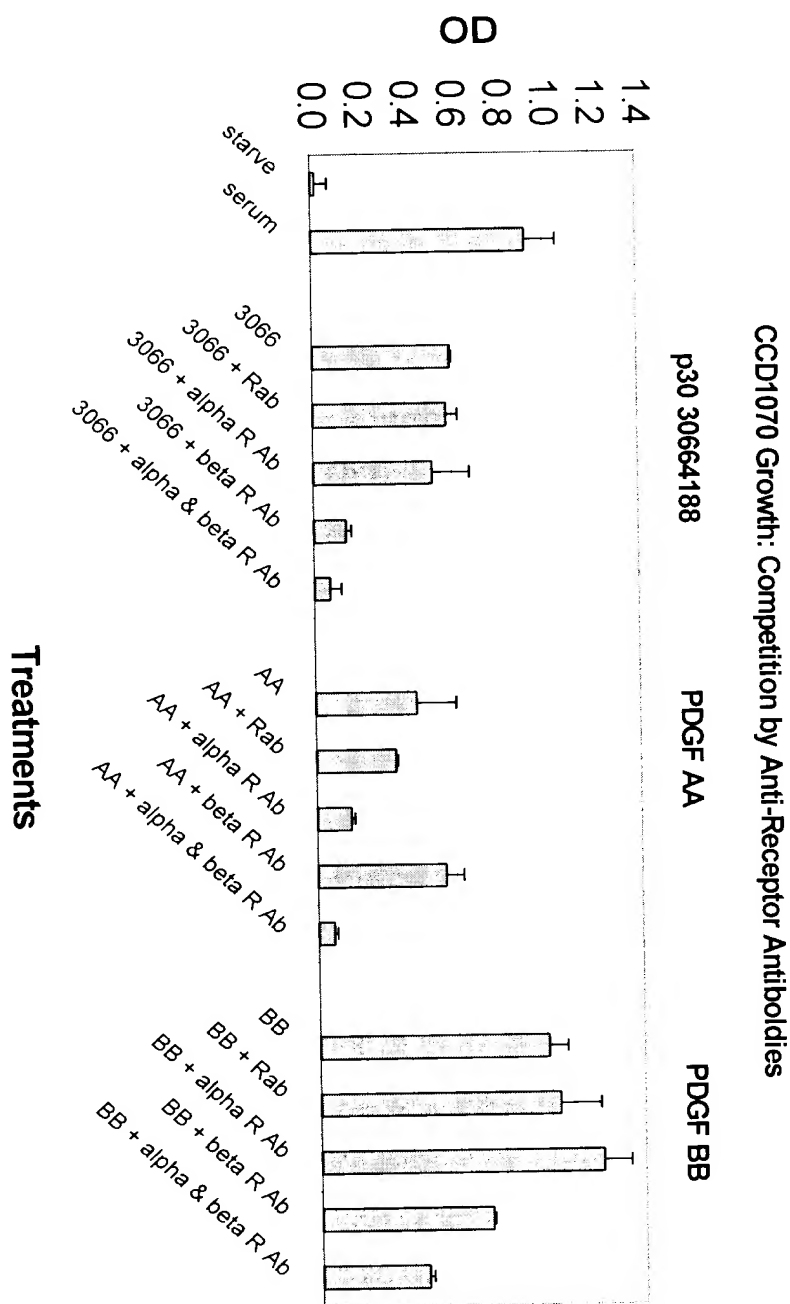


FIG. 21

Smooth Muscle Treated with p30 30664188, PDGF AA, PDGF BB

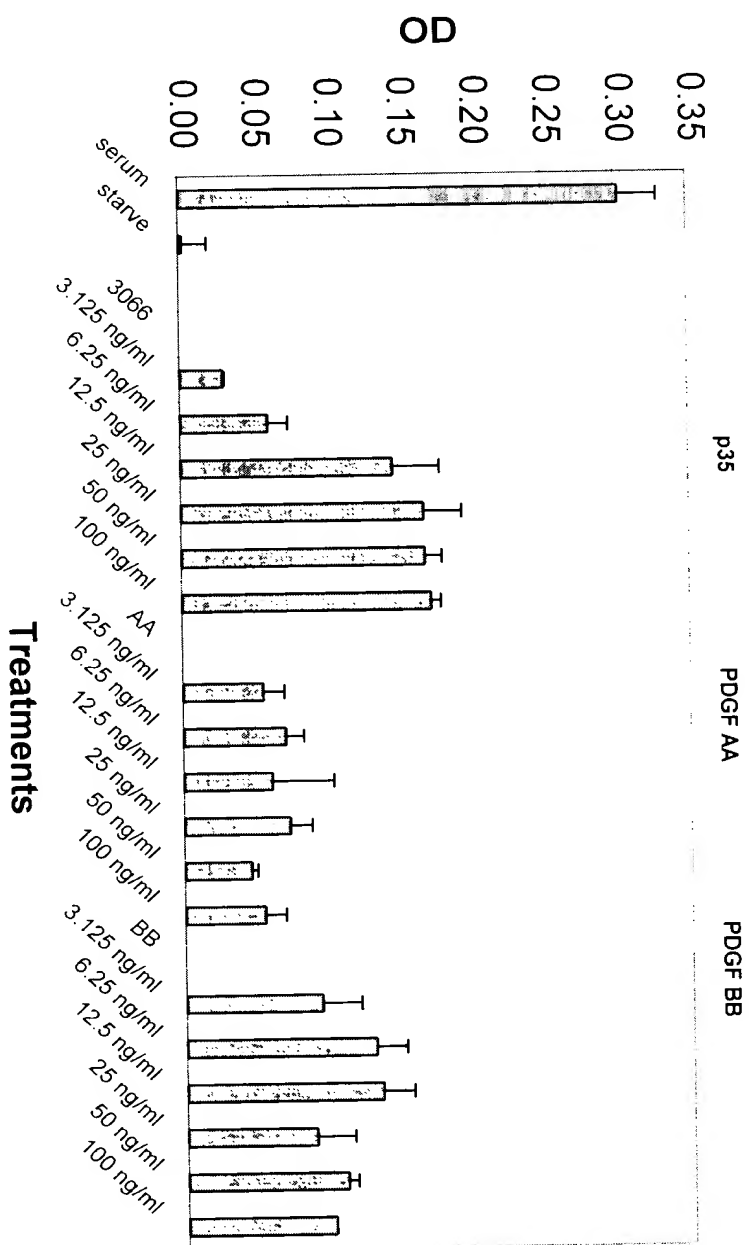


FIG. 22

Smooth Muscle Cell Proliferation

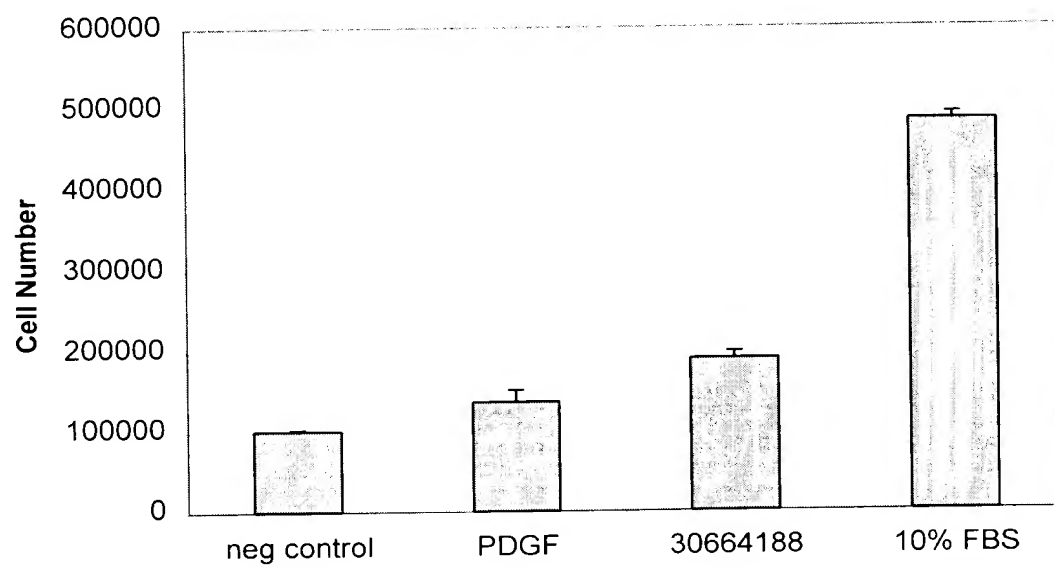


FIG. 23

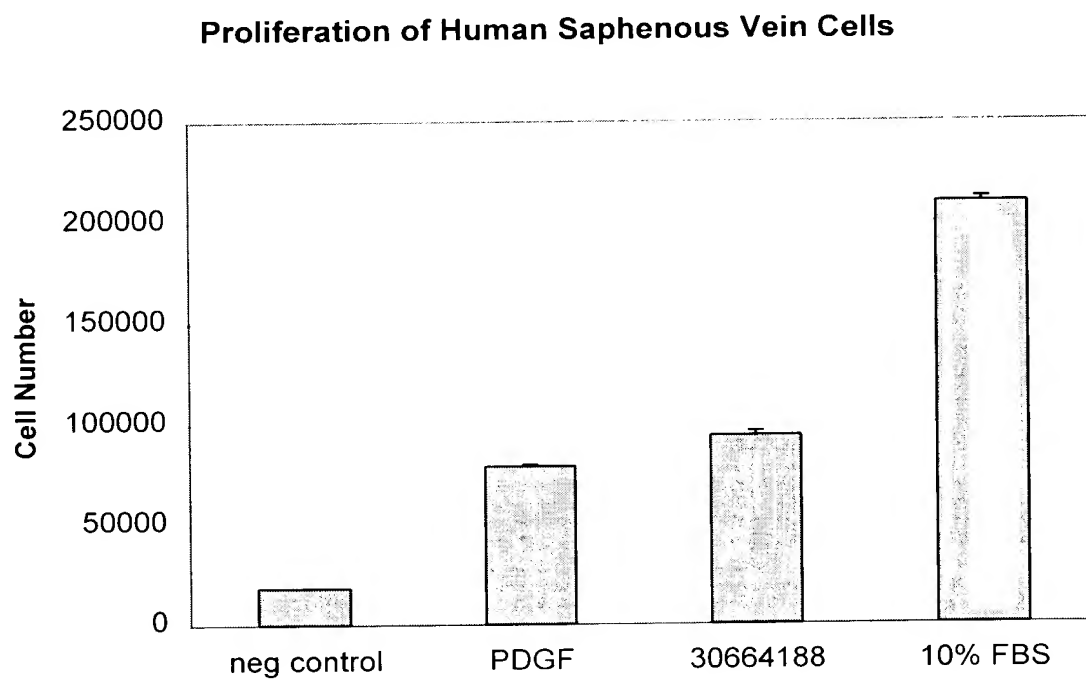


FIG. 24

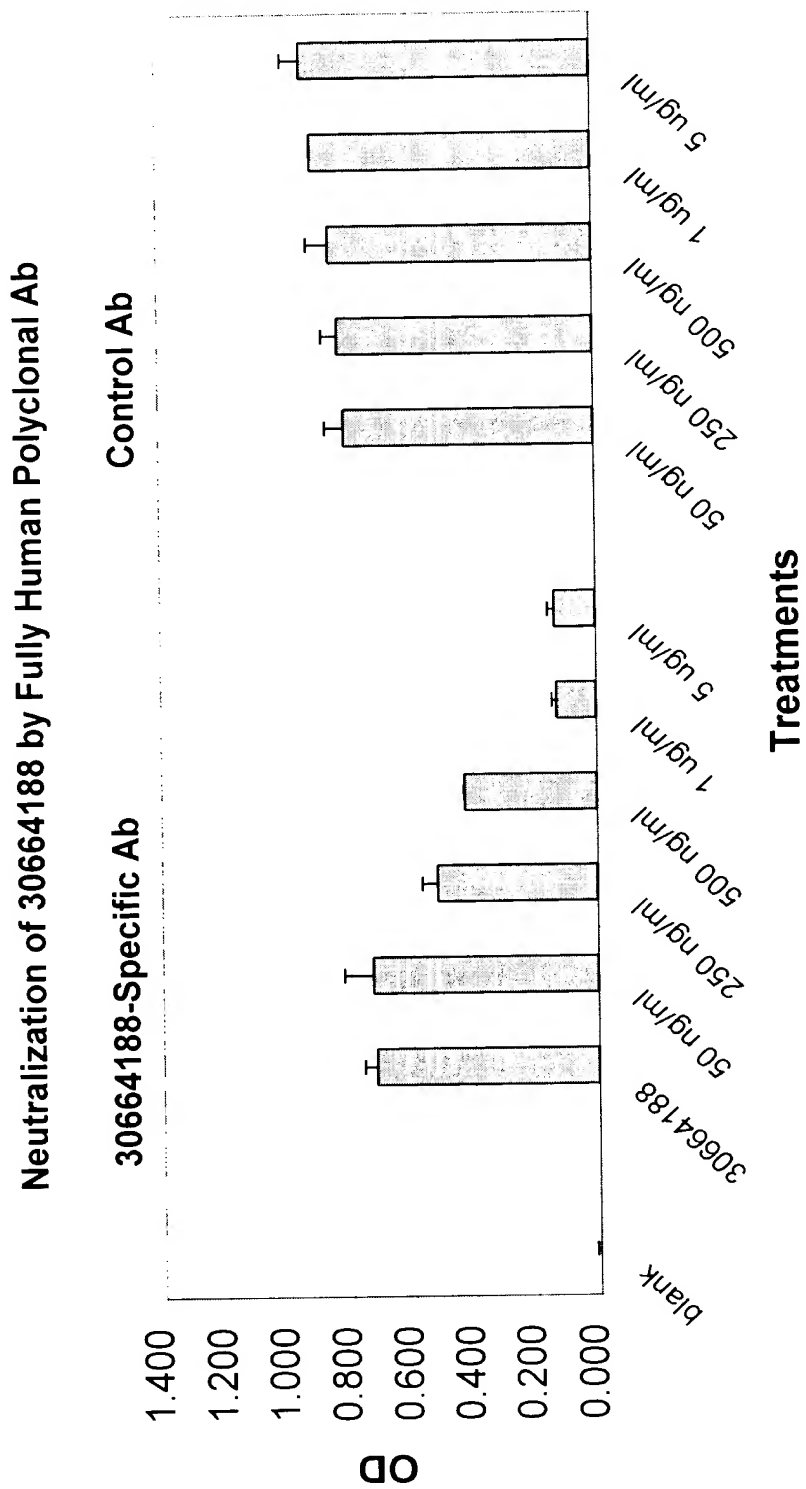


Fig. 25.

Panel A

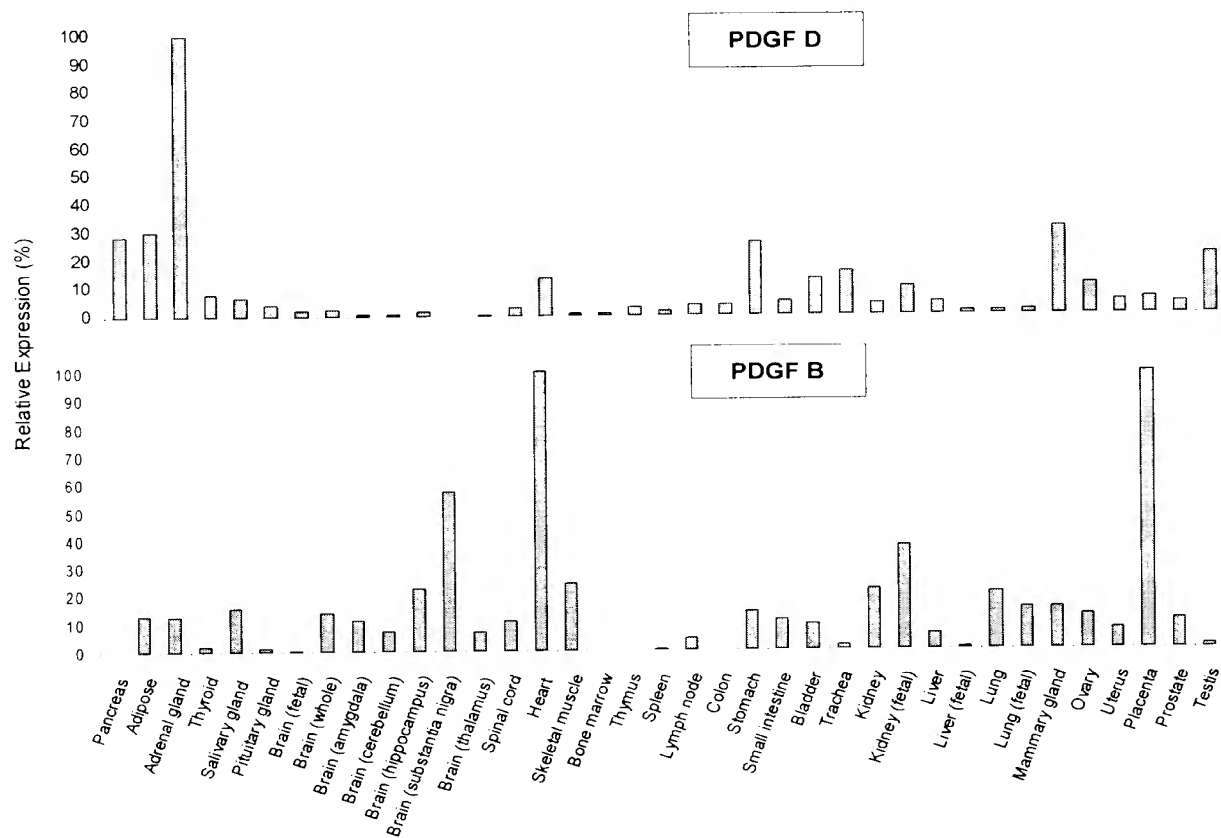


Fig. 25 (cont.)

Panel B

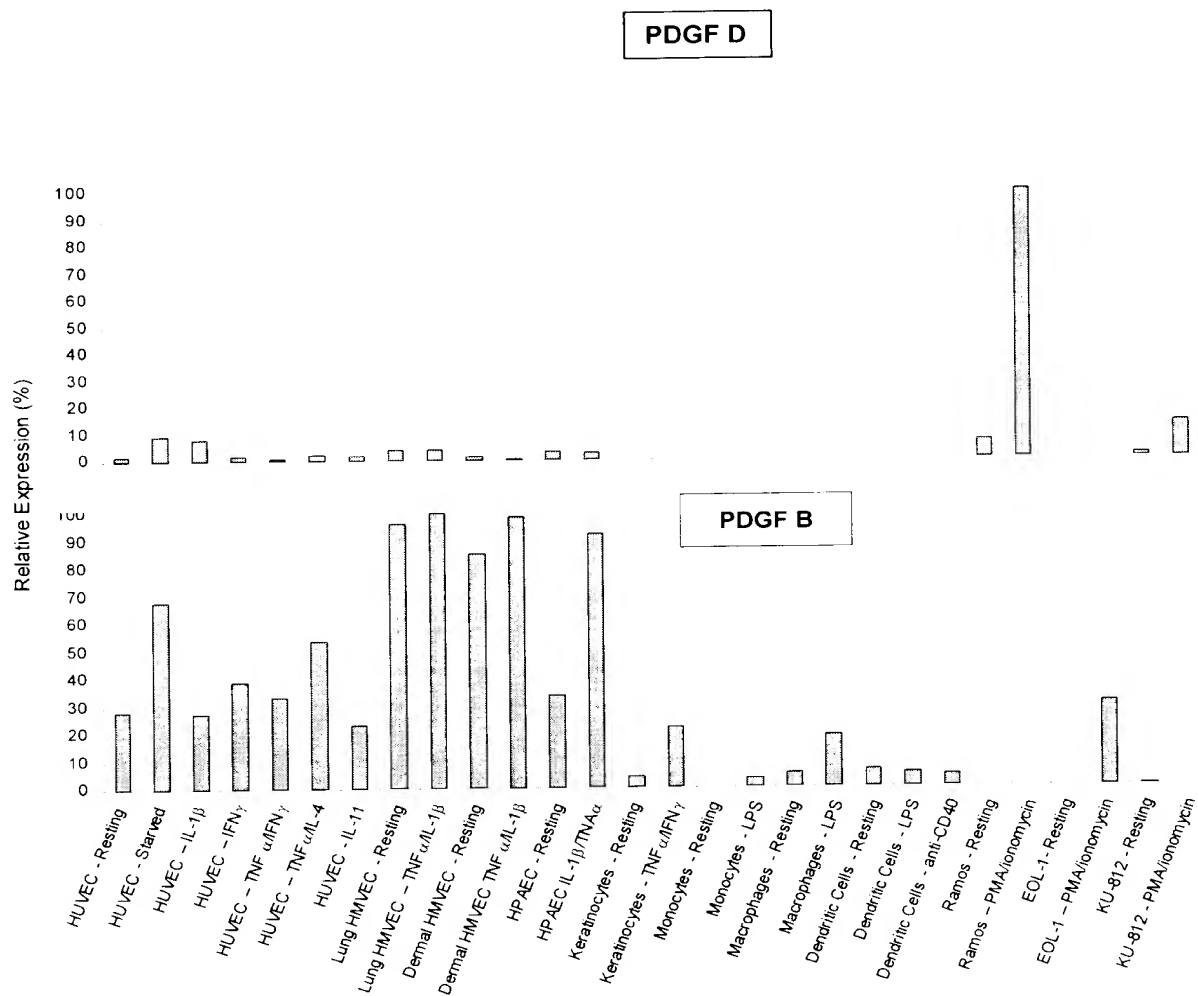


FIG. 26.

BrdU CCD1070 Soluble Alpha PDGFR Competition

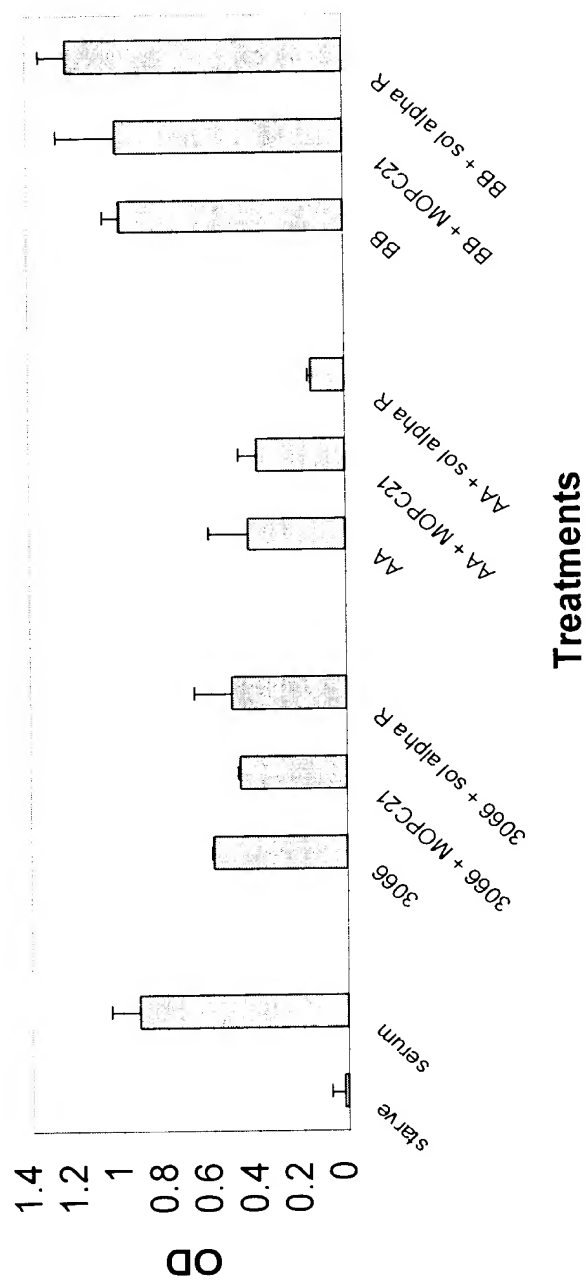


FIG. 27A

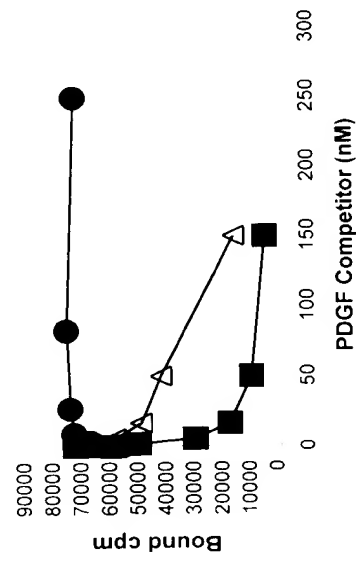


FIG. 27B

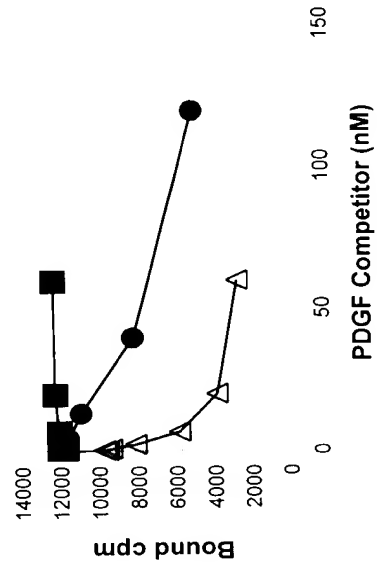


FIG. 28

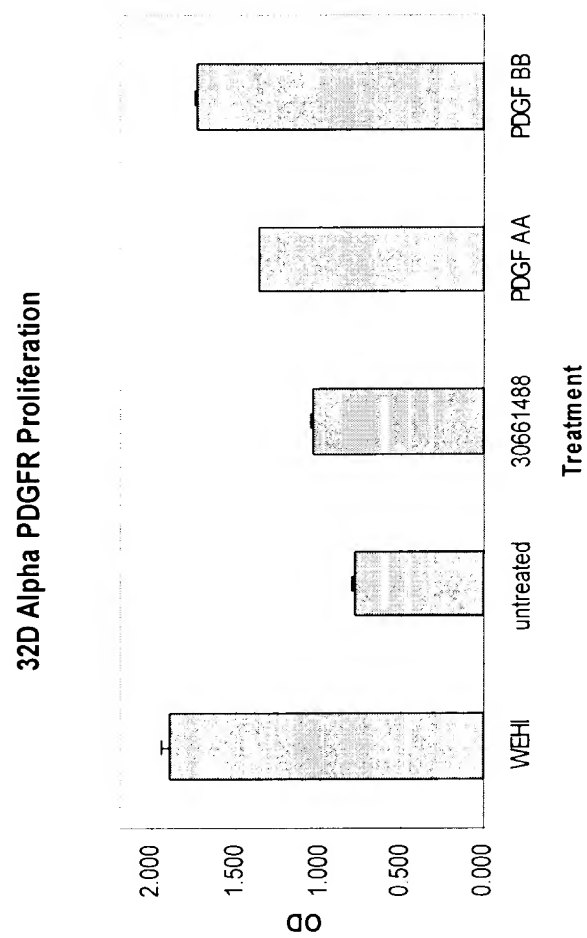


FIG. 29A

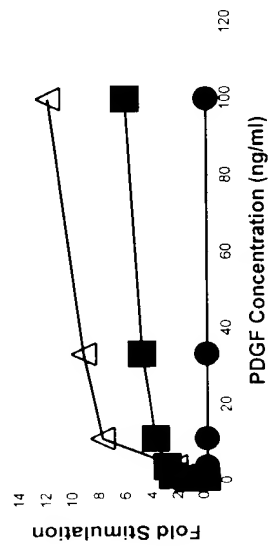


FIG. 29B

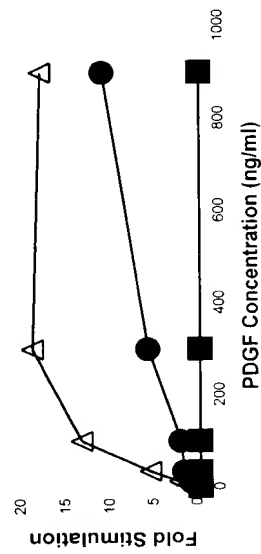


FIG. 29C

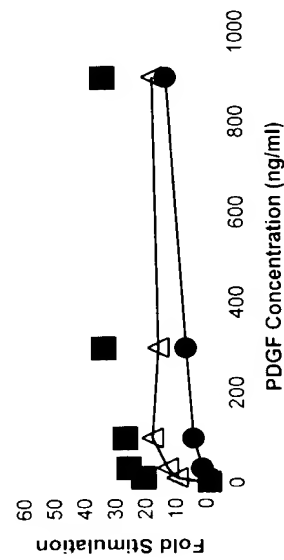


FIG. 29D

